

SUMMARIES

Description

(without alignments)
117.112 Million cell updates/sec

Sequence: 1 aggcctcgcgaggaacgcgtgtcccatgtccaact 34

Gapop 10.0 , Gapext 1.0

Total number of hits satisfying chosen parameters: 4109280

Maximum DB seq Length: 20000000000

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Post-processing: Minimum Match 08
                  Maximum Match 1008
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Listing first 45 summaries

Database :

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2:  qb.hrg: *
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6:  qb.pat: *
7:  qb.ph: *
8:  qb.pl: *
9:  qb.pr: *
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23:  em.pat: *
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27:  em.sts: *
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34:  em.hrg_pln: *
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39:  em.hrgo_hum: *
40:  em.hrgo_mus: *
41:  em.hrgo_other: *

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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	DB	ID	Description
1	34	100.0	847	9	HSINHAJ2	X04446 H.sapiens i
2	34	100.0	1134	6	A14420	A14420 Inhibin A s
3	34	100.0	1237	6	101843	101843 Sequence 10
4	34	100.0	1237	6	105264	105264 Sequence 21
5	34	100.0	1237	6	121913	121913 Sequence 40
6	34	100.0	1237	6	164619	164619 Sequence 40
7	34	100.0	1237	6	187901	187901 Sequence 40
8	34	100.0	1237	6	M13144	Human ovary
9	34	100.0	1338	6	100529	Sequence 1
10	34	100.0	1338	9	HOMINHA	M13981 Human inhib
11	34	100.0	1393	9	BC006391	Human sapi
12	34	100.0	53239	2	AC011971	AC011971 Homo sapi
13	34	100.0	135033	5	AC009955	AC009955 Homo sapi
14	34	100.0	182662	2	AC024009	AC024009 Homo sapi
15	34	100.0	186883	2	AC040991	AC040991 Homo sapi
16	27.6	81.2	994	4	EC021219	U21219 Equus caball
17	27.6	81.2	1286	4	HRS1ASP	D50327 Horse mRNA
18	27.6	81.2	1372	10	AF432551	AF432551 Phodopus
19	26	76.5	857	4	SHP1NHA	L28815 Sheep inhib
20	26	76.5	1144	10	RATINBMB2	M32755 Rat inhibin
21	26	76.5	1160	10	MMINAS	X55957 M.musculus
22	26	76.5	1182	4	BOVINHA	M13373 Bovine inh
23	26	76.5	1182	6	A14416	A14416 Inhibin A s
24	26	76.5	1183	10	MUSINHD02	M95525 Mouse inhib
25	26	76.5	1328	10	MNALPHA	X66618 M.musculus
26	26	76.5	1361	10	RATINHA	M36453 Rat inhibin
27	26	76.5	101356	2	AC112361	AC112361 Rattus no
28	24.4	71.8	731	4	AY028465	AY028465 Sus scrofa
29	24.4	71.8	731	4	AY028466	AY028466 Sus scrofa
30	24.4	71.8	1272	4	PIGINHA	M13980 Pig inhibin
31	24.4	71.8	1333	4	SININHA	X03265 Porcine mRN
32	24.4	71.8	1343	6	101835	101835 Sequence 2
33	24.4	71.8	1343	6	105231	105231 Sequence 13
34	24.4	71.8	1343	6	121910	121910 Sequence 30
35	24.4	71.8	1343	6	164616	164616 Sequence 30
36	24.4	71.8	1343	6	187898	187898 Sequence 30
37	22.6	66.5	180525	2	AC104750	AC104750 Mus muscu
38	21.8	64.1	11158	1	AE004682	AE004682 Pseudomon
39	21.8	64.1	118051	2	AC130781	AC130781 Rattus no
40	21.8	64.1	240568	2	AC098942	AC098942 Rattus no
41	21.4	62.9	84780	9	AC005885	AC005885 Homo sapi
42	21.4	62.9	150735	9	AC090687	AC090687 Homo sapi
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44	21.4	62.9	237982	2	AC039483	AC039483 Mus muscu
45	21.2	62.4	140069	2	AC107245	AC107245 Rattus no

ALIGNMENTS

RESULT 1			
HSINHAG2			
LOCUS	847 bp	inA	linear
DEFINITION	H sapiens inA gene, exon 2.		
ACCESSION	X04446		
VERSION	X04446.1 GI:33924		
KEYWORDS	glycoprotein; glycoprotein hormone; hormone; inhibin;		

SOURCE ORGANISM

REFERENCE
AUTHORS

1 (bases 1 to 847)
Stewart, A.G., Milborrow, H.M., Ring, J.M., Crowther, C.E. and
Forage, R.G.

TITLE Human inhibin genes. Genomic characterisation and sequencing
JOURNAL FEBS Lett. 206 (2), 329-334 (1986)
MEDLINE 87005283
PubMed 3758355

COMMENT See x04445 for exon 1.
Data kindly reviewed (05-JAN-1986) by Stewart A.

FEATURES Location/Qualifiers

source

1..847

gene /organism="Homo sapiens"

exon /db_xref="taxon:9606"

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number=2 /usedin=X04445:inh_cds

/usedin=X04445:inh_mat

/usedin=X04445:inh_mrna

172..174

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538..540 /gene="inhA"

/note="pot. N-glycosylation site"

640..642 /gene="inhA"

/note="pot. N-glycosylation site"

misc_feature /note="pot. N-glycosylation site"

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Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGGCTGCCATGCCACT 34

Db 487 AGGCTCGGAGAACCGGCTGCCATGCCACT 520

RESULT 2

LOCUS A14420

DEFINITION Inhibin A subunit.

ACCESSION A14420

VERSION A14420.1 GI:490129

KEYWORDS

SOURCE

ORGANISM

FEATURES

source

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/organism="Homo sapiens"

/db_xref="taxon:9606"

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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGGCTGCCATGCCACT 34

Db 758 AGGCTCGGAGAACCGGCTGCCATGCCACT 791

RESULT 3

LOCUS 101843

DEFINITION Sequence 10 from Patent US 4798865.

ACCESSION 101843

VERSION 101843.1 GI:269775

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1237)

Authors Mason, A.J. and Seeburg, P.H.

Compositions of hormonally active human and porcine inhibin

containing an alpha chain and 62 chain

Patent: US 4798865-A, 10 17 JAN 1989,

Genentech, Inc., South San Francisco, CA

FEATURES

source

/organism="unknown"

BASE COUNT 210 a 431 c 346 g 250 t

ORIGIN

Query Match 100.0%; Score 34; DB 6; Length 1237;

Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGGCTGCCATGCCACT 34

Db 708 AGGCTCGGAGAACCGGCTGCCATGCCACT 741

RESULT 4

LOCUS 105264

DEFINITION Sequence 21 from Patent EP 0222491.

ACCESSION 105264

VERSION 105264.1 GI:591394

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 (bases 1 to 1237)

Authors Mason, A.J. and Seeburg, P.H.

Nucleic acid encoding the alpha or beta chains of inhibin and

method for synthesizing the polypeptides using such nucleic acid

Patent: EP 0222491-A1 21 20 NOV 1987;

Location/Qualifiers

1..1237

/organism="unknown"

BASE COUNT 210 a 431 c 346 g 250 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.017;

Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGGAGAACCGGCTGCCATGCCACT 34

Db 708 AGGCTCGGAGAACCGGCTGCCATGCCACT 741

RESULT 5

LOCUS 121913

DEFINITION Sequence 40 from patent US 5523488.

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ACCESSION 121913
VERSION 121913.1 GI:1602267
KEYWORDS
SOURCE Unknown
ORGANISM Unclassified
REFERENCE 1 (bases 1 to 1237)
AUTHORS Mason,A.J., and Seeburg,P.H.
TITLE Nucleic acid encoding the mature .alpha. chain of inhibin and
method for synthesizing polypeptides using such nucleic acid
JOURNAL Patent: US 5525488-A 40 11-JUN-1996;
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BASE COUNT  210 a  431 c  346 g  250 t
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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGAACCGCGCCGATGCCACT 34
Db 708 AGGCTCCGAGAACCGCGCTGCCATGCCACT 741

RESULT 6
LOCUS 164619 1237 bp DNA linear PAT 07-OCT-1997
DEFINITION Sequence 40 from patent US 5665568.
ACCESSION 164619
VERSION 164619.1 GI:2481513
KEYWORDS
SOURCE Unknown
ORGANISM Unclassified
REFERENCE 1 (bases 1 to 1237)
AUTHORS Mason,A.J., and Seeburg,P.H.
TITLE Nucleic acid encoding the mature .beta. sub.A chain of inhibin and
method for synthesizing polypeptides using such nucleic acid
JOURNAL Patent: US 5665568-A 40 09-SEP-1997;
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BASE COUNT  210 a  431 c  346 g  250 t
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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 708 AGGCTCCGAGAACCGCGCTGCCATGCCACT 741

RESULT 7
LOCUS 187901 1237 bp DNA linear PAT 10-AUG-1998
DEFINITION Sequence 40 from patent US 5716810.
ACCESSION 187901
VERSION 187901.1 GI:3407841
KEYWORDS
SOURCE Unknown
ORGANISM Unclassified
REFERENCE 1 (bases 1 to 1237)
AUTHORS Mason,A.J., and Seeburg,P.H.
TITLE Nucleic acid encoding the mature .beta. sub.B chain of inhibin and
method for synthesizing polypeptides using such nucleic acid
JOURNAL Patent: US 5716810-A 40 10-FEB-1998;
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BASE COUNT  210 a  431 c  346 g  250 t
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Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGAACCGCGCTGCCATGCCACT 34
Db 708 AGGCTCCGAGAACCGCGCTGCCATGCCACT 741

RESULT 8
LOCUS HUMINHAA 1247 bp mRNA linear PRI 06-JAN-1995
DEFINITION Human ovarian alpha-inhibin mRNA.
ACCESSION M3144
VERSION M3144.1 GI:186412
KEYWORDS Human polycystic ovarian cDNA to mRNA, c-myc-lambda-hin-alpha-
(12.6).
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Plimates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 1247)
AUTHORS Mason,A.J., Niall,H.D., and Seeburg,P.H.
TITLE Structure of two human ovarian inhibins
JOURNAL Biochem. Biophys. Res. Commun. 135 (3), 957-964 (1986)
MEDLINE 86186863
PUBMED 3754442
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BASE COUNT  210 a  431 c  346 g  250 t
ORIGIN romosome 2q33-qter.
Query Match          100.0%; Score 34; DB 9; Length 1237;
Best Local Similarity 100.0%; Pred. No. 0.017;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCCGAGAACCGCGCTGCCATGCCACT 34
Db 708 AGGCTCCGAGAACCGCGCTGCCATGCCACT 741

RESULT 9
LOCUS 100529 1338 bp ss-DNA linear PAT 21-MAY-1993
DEFINITION Sequence 1 from Patent US 4737578.
ACCESSION 100529
VERSION 100529.1 GI:768923
KEYWORDS
SOURCE Unknown
ORGANISM Unknown

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Unclassified.

REFERENCE 1 (bases 1 to 1338)
 AUTHORS Evans, R.M., Rosenfeld, M.G., Cerelli, J.G., Mayo, K.E., Spiess, J.,
 Rivier, J.E.F., and Vale, W.W., Jr.
 TITLE Human Inhibin
 JOURNAL Patent: US 4737578-A 1 [4-Apr-1988;
 The Salk Institute for Biological Studies; San Diego, CA

FEATURES
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Query Match 100.0%; Score 34; DB 9; Length 1338;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 10
 HUMANHA 1338 bp mRNA linear PRI 06-JAN-1995
 LOCUS
 DEFINITION Human inhibin A-subunit mRNA, complete cds.
 ACCESSION M13981
 VERSION M13981.1 GI:186410
 KEYWORDS inhibin.
 SOURCE Human term placenta, cDNA to mRNA, clone hESA-110.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1338)
 AUTHORS Mayo, K.E., Cerelli, J.G.M., Spiess, J., Rivier, J., Rosenfeld, M.G.,
 Evans, R.M., and Vale, W.
 TITLE Inhibin A-subunit cDNAs from porcine ovary and human placenta
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 83 (16), 5849-5853 (1986)
 MEDLINE 86287350
 PubMed 3016724

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Unclassified.

REFERENCE 1 (bases 1 to 1338)
 AUTHORS Evans, R.M., Rosenfeld, M.G., Cerelli, J.G., Mayo, K.E., Spiess, J.,
 Rivier, J.E.F., and Vale, W.W., Jr.
 TITLE Human Inhibin
 JOURNAL Patent: US 4737578-A 1 [4-Apr-1988;
 The Salk Institute for Biological Studies; San Diego, CA

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 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query Match 100.0%; Score 34; DB 9; Length 1338;
 Best Local Similarity 100.0%; Pred. No. 0.016;
 Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 11
 BC006391 1393 bp mRNA linear PRI 12-JUL-2001
 LOCUS
 DEFINITION Homo sapiens, inhibin, alpha, clone MGC:12547 IMAGE:4126990, mRNA,
 complete cds.
 ACCESSION BC006391
 VERSION BC006391.1 GI:13623556
 KEYWORDS MGC.
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 REFERENCE 1 (bases 1 to 1393)
 AUTHORS Strausberg, R.
 TITLE Direct Submission
 JOURNAL Submitted (09-APR-2001) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: <http://mgc.nci.nih.gov>
 Contact: MGC help desk
 Email: cgabs-rt@mail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The J.M.A.G.E. Consortium (J.M.N.)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (MGC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mgc@nih.gov
 Shvachenko, Y., Welberry, K.D., Beckstrom, Sternberg, S.M.,
 Benjamin, B., Blakesley, R.W., Boultard, G.G., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,
 Lim, M., Maduro, Q.L., Mastello, C., Mestrian, S.D., McCloskey, J.C.,
 McGowell, J.L., Pearson, R., Snyder, B., Stanitrop, S., Thomas, P.J.,
 Tongson, E.E., Touchman, J.W., Turgeon, C., Vogt, J.L., Walker, M.A.,
 Zhang, L.-H., and Green, E.D.
 Clon distribution: MGC clone distribution information can be found
 through the J.M.A.G.E. Consortium/CLIN.cgi: <http://Image.jnl.gov>
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 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA GI: 9257223.
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Query Match 100.0%; Score 34; DB 9; Length 1933;
Best Local Similarity 100.0%; Pred. No. 0.016;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGGCTCGAGAGACGGTGGCCATGCCACT 34
|||||
Db 840 AGGCTCGAGAGACGGCTGCCATGCCACT 873

RESULT 12
AC011971
LOCUS Homo sapiens clone RP11-15J2, LOW-PASS SEQUENCE SAMPLING.
DEFINITION AC011971
AC011971 2 GI:7144910
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 53239)
Britten, B., Linton, L., Nusbaum, C. and Lander, E.
Homo sapiens chromosome, clone RP11-15J2
Unpublished
2 (bases 1 to 53239)
Britten, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M.,
Baldwin, J., Barna, N., Beckert, R., Boguslavsky, I., Bouckgatter, B.,
Brown, A., Castle, A., Colangelo, M., Collins, S., Collamore, A.,
Cooke, P., DeArliano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M.,
Ferreira, P., Fitzhugh, W., Forrest, C., Funke, R., Gage, D.,
Galagan, J., Garday, S., Grant, G., Hagos, B., Heaford, A., Horton, L.,
Howland, J.C., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J.,
Lehoczky, J., Liu, C., Locke, K., MacDonald, P., Marquis, N.,
McMan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrum, J.,
Morrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P.,
Peterson, K., Pollara, V., Riley, R., Roy, A., Santos, R., Severy, P.,
Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,
Tesfaye, S., Tifrell, A., Vassiliev, H., Vo, A., Wheeler, J., Wu, X.,
Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
Direct Submission
Submitted (17-OCT-1999) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Mar 3, 2000 this sequence version replaced 91:6065396.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: W18R
Web site: <http://www-seq.wi.mit.edu>
Contact: sequence.submissions@genome.wi.mit.edu
----- Project Information -----
Center project name: L3480
Center clone name: 15_12

* NOTE: This record contains 59 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.

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* 4534 5313: contig of 780 bp in length
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* 10685 10784: gap of 100 bp
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* 11764 12573: contig of 810 bp in length
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* 14467 15278: contig of 812 bp in length
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* 16287 16977: contig of 691 bp in length
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* 17078 17860: contig of 783 bp in length
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* 17961 18841: contig of 881 bp in length
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* 20661 21354: contig of 694 bp in length
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* 21455 22269: contig of 815 bp in length
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* 22370 23163: contig of 794 bp in length
* 23164 23263: gap of 100 bp
* 23264 24012: contig of 745 bp in length
* 24013 24112: gap of 100 bp
* 24113 24884: contig of 772 bp in length
* 24885 24984: gap of 100 bp
* 24985 25780: contig of 796 bp in length
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* 25881 26672: contig of 792 bp in length
* 26673 26772: gap of 100 bp
* 26773 27626: contig of 854 bp in length
* 27627 27726: gap of 100 bp
* 27727 28587: contig of 861 bp in length
* 28588 28687: gap of 100 bp
* 28688 29501: contig of 814 bp in length
* 29502 29601: gap of 100 bp
* 29602 30332: contig of 731 bp in length
* 30333 30432: gap of 100 bp
* 30433 31215: contig of 783 bp in length
* 31216 31315: gap of 100 bp
* 31316 32153: contig of 838 bp in length
* 32154 32253: gap of 100 bp
* 32254 32926: contig of 673 bp in length
* 32927 33026: gap of 100 bp
* 33027 33815: contig of 789 bp in length
* 33816 33915: gap of 100 bp
* 33916 34761: contig of 846 bp in length
* 34762 34861: gap of 100 bp
* 34862 35683: contig of 822 bp in length

Overlap. Actual start of this clone is at base position 1 of
RP11-256123; actual end is at base position 52326 of RP11-51207.

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Db 46065 AGGCTCGGAGCAACCGCCGCGACGACCT 46098

RESULT 14
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VERSION AC024009.2 GI:7210067
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SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE
1 (bases 1 to 182662)
Birken,B., Linton,L., Nussbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 2, clone RP11-158J14
JOURNAL Unpublished
REFERENCE
2 (bases 1 to 182662)
Birken,B., Linton,L., Nussbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barina,N., Bede,F., Boguslavsky,L.,
Boukhalil,B., Brown,A., Burkett,G., Campopiano,A., Castle,A.,
Chapel,Y., Colangelo,M., Collins,S., Collimore,A., Cooke,P.,
Dearellano,K., Dewar,K., Dodge,S., Domino,M., Doyle,M.,
Fenster,J., Ferreira,P., Fitzhugh,M., Forrest,C., Gage,D.,
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Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Landers,T., Laroque,K., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N., McCarthy,M., McEwan,P., McGuirk,A., McKernan,K., McPheeters,R., Meldrum,J., Menes,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.N., Peterson,K., Pierre,N., Pisanli,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,J., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zalnoun,J., Zimmer,A. and Zody,M.

TITLE
JOURNAL
REFERENCE
AUTHORS

Direct Submission
 Submitted (20-FEB-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 3 (bases 1 to 182662)

Birken,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Beda,F., Boguslavsky,L., Bouckhalter,B., Brown,A., Burkett,G., Campoliano,A., Castle,A., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cooke,P., DeArrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domingo,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Laroque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., Macdonald,P., Margulis,N., McCarthy,M., McEwan,P., McGuirk,A., McKernan,K., McPheeters,R., Meldrum,J., Menes,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,T.N., Oliver,J., Peterson,K., Pierre,N., Pisanli,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schauer,S., Severy,J., Stojanovic,N., Subramanian,A., Talamas,J., Testaye,S., Theodore,J., Travers,M., Triggillo,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zalnoun,J., Zimmer,A. and Zody,M.

TITLE
JOURNAL
COMMENT

Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
 On Mar 8, 2000 this sequence version replaced g173008914.
 All repeats were identified using RepeatMasker:
 Smit, A.F.A. & Green, P. (1996-1997)
 http://ftp.genome.washington.edu/RW/repeatMasker.html

----- Genome Center -----
 Center: Whitehead Institute/ MIT Center for Genome Research
 Center code: WIRB
 Web site: http://www-seq.wi.mit.edu
 Contact: sequence_submissions@genome.wi.mit.edu
 ----- Project Information -----
 Center project name: L7216
 Center clone name: 158.J.14
 ----- Summary Statistics -----
 Sequencing vector: M13; M77815; 100% of reads
 Chemistry: dye-terminator Big Dye; 100% of reads
 Assembly program: Phrap; version 0.96071
 Consensus quality: 162604 bases at least Q40
 Consensus quality: 171836 bases at least Q30
 Consensus quality: 176600 bases at least Q20
 Insert size: 180000; agarose-1p
 Insert size: 179762; sum-of-ctrls
 Quality coverage: 3.9 in Q20 bases; agarose-1p
 Quality coverage: 3.9 in Q20 bases; sum-of-ctrls

 * NOTE: This is a 'working draft' sequence. It currently
 * consists of 30 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will

* be preserved.

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DB 90614 AGGCTCCGAGAACCGCTGCCATGCCAACT 90647

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DEFINITION SEQUENCE. 17 unordered pieces.
ACCESSION AC040991.2 GI:8014664
VERSION HTG: HTGS_PHASE1; HTGS_DRAFT.
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 186883)
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.
TITLE Homo sapiens chromosome 2, clone RP11-123E11
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 186883)
AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N.,
Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F.,
Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G.,
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Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P.,

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TITLE
JOURNAL
REFERENCE
AUTHORS
Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 186883)

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O'Neil,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanil,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schanauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Tajimas,J., Testaye,S., Theodore,J., Tirrell,A., Travers,M., Triggilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (11-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 186883)

Birren,B., Linton,L., Nusbaum,C., Lander,E., Abraham,H., Allen,N., Anderson,S., Baldwin,J., Barna,N., Bastien,V., Bida,F., Boguslavsky,L., Boukhgalter,B., Brown,A., Burkett,G., Campopiano,A., Castle,A., Choquet,Y., Colangelo,M., Collins,S., Collamore,A., Cooke,P., Dearellano,K., Dewar,K., Diaz,J.S., Dodge,S., Domino,M., Doyle,M., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S., Glade,S., Goyette,M., Graham,L., Grand-Pierre,N., Grant,G., Hagos,B., Heatford,A., Horton,L., Howland,J.C., Iliev,I., Johnson,R., Jones,C., Kann,L., Karatas,A., Klein,J., Lacroque,K., Lamazares,R., Landers,T., Lehoczy,J., Levine,R., Lieu,C., Liu,G., Locke,K., MacDonald,P., Marquis,N., McCarthy,M., McKean,P., Mccurt,A., McKernan,K., Mcpheeters,R., Meitrim,D., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Olivari,T.M., Oliver,J., Peterson,K., Pierre,N., Pisanil,C., Pollara,V., Raymond,C., Riley,R., Rogov,P., Rothman,D., Roy,A., Santos,R., Schanauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Tajimas,J., Testaye,S., Theodore,J., Tirrell,A., Travers,M., Triggilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zimmer,A. and Zody,M.

Direct Submission

Submitted (12-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

On May 22, 2000 this sequence version replaced g1:7534193.

All repeats were identified using RepeatMasker:

Smith, A.P.A. & Green, P. (1996-1997)

http://ftp.genome.washington.edu/RM/RepeatMasker.html

----- Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIR

Web site: <http://www-seq.wi.mit.edu>

Contact: sequence_submissions@genome.wi.mit.edu

----- Project Information

Center project name: 19492

Center clone name: 124_E_11

----- Summary Statistics

Sequencing vector: R33 M77815: 100% of reads

Chemistry: Dye-Termination Big Dye3 100% of reads

Assembly program: Phrap: version 0.960731

Consensus quality: 175185 bases at least Q40

Consensus quality: 181490 bases at least Q30

Consensus quality: 183848 bases at least Q20

Insert size: 190000; agarose-fp

Insert size: 185283; sum-of-contigs

Quality coverage: 4.3 in Q20 bases; agarose-fp

Quality coverage: 4.4 in Q20 bases; sum-of-contigs

NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

```

1 1462: contig of 1462 bp in length
* 1463 1562: gap of 100 bp
* 1563 4486: contig of 2924 bp in length
* 4487 4586: gap of 100 bp
* 4587 9251: contig of 4665 bp in length
* 9252 9351: gap of 100 bp

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BASE COUNT      12272 a   51993 c   50651 g   40377 t   1610 others
ORIGIN
Query Match      100.0%; Score 34; DB 2; Length 186883;
Best Local Similarity 100.0%; Pred. No. 0.012;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY      1 AGAGCTCCGAGAGGAGGCTGCTGCTGCTGCACT 34
          |||||
Db 105583 AGAGCTCCGAGAGGAGGCTGCTGCTGCTGCACT 105583
Search completed: March 11, 2003, 09:19:22
Job time : 8545.13 secs

```